

SEQ ID NO:1

FIGURE 1

CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCCTGGTGGTTTCTGTTTCCTGAAGGA
AGTGACGGGGGGTGGGATTGAATGAAAAGTGCAAAACACAGGCTCGCAGCGCTGGA
GCCCCGGGGCCGCGGAGCCGGGCGGGGCAGCGCCGTCTCCGCCTCGGGGCGCCCGG
GGGCGCCCTGCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCG
CGGCCAAGGCCCCCGGCGGAGCGGCTCCCGGGCGCCCCGAAGTAGCCCCCAACTTT
GGGCGAAGTTTGCCTGCGCCTCTCCCCGCCCCACGCGGCGCGCCGGGGCCGCGGA
CGGCAGCGGCCCCCGGGGATGCGCCTTCCCGGGGTACCCCTGGCGCGCCCTGCGCT
GCTGCTGCTGCTGCCGCTGCTCGCGCCGCTGCTGGGAACGGGTGCGCCGGCCGAGCT
GCGGGTCCGCGTGCGGCTGCCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGG
ACAGCGACGCGGACAGCATCAGCCTCGAGCTGCGCAAGCCCGACGGCACCCCTCGTC
TCCTTCACCGCCGACTTCAAGAAGGATGTGAAGGTCTTCCGGGGCCCTGATCCTGGGG
GAGCTGGAGAAGGGGCAGAGTCAGTTCAGGGCCCTCTGCTTTGTCACCCAGCTGCA
GCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGGCAGAAAAATCCCC
GGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGAATGTC
GCTGTCAACTTCAGCCAGGGGGCCCTGCTGAGCCCCCATCTCCACAACGTGTGTGCC
GAGGCCGTGGATGCCATCTACACCCGCCAGGAGGATGTCCGGTTCTGGCTGGAGCA
AGGTGTGGACAGTTCTGTGTTTCGAGGCTCTGCCCAAGGCCTCAGAGCAGGCGGAGC
TGCCTCGCTGCAGGCAGGTGGGGGACCGCGGGAAGCCCTGCGTCTGCCACTATGGC
CTGAGCCTGGCCTGGTACCCCTGCATGCTCAAGTACTGCCACAGCCGCGACCGGGCCC
ACGCCCTACAAGTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTAC
GTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTACCCAGGCTAGGGTGG
GAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCCACTGCTCTTACCAGCCACTAGAGG
GGGTGGCAACCCCCACCTGAGGCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTA
GAGCCTGGGGCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCATGGCA
GGGGGTCTCATGAAGGCACCCCCATTCCCACCCTGTGCCTTCCTTGCGGGCAGAGAG
GGAGAGAAGGGCTCCCCAGATCTACACCCCTCCCTCCTGCATCTCCCCTGGAGTGTT
CACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAAC
GTTTAGACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACAACTCCC
TTCCCCATGCACACATCTGGAAGGAGCTGGCCCCCTCAGTCCCTTCCTACTCCCCAAC
AAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTG
TACTGGATTACAGCATATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGG
AGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCCTTCCCGGACCTGGAC
GTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAA
GGTTCTGGGGCAGGGAGGGAGCATGAAGTACGAGGAAAACCTGAATTCCAGATTTT
TAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTTAAGTTTTTACTTGACT
AATGAGACCCAGAGTTTGGAGAAAACCTTTTGCCAATGCTGCCACCTGATGTCAGA
AAGTGTCCCCACACCCTAGCAGTGGCCTATCTTGGAACAAGAACTTCGAAAGCACCT

[illegible]

ACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGA
AGGATGAGATAAACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGT
AGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGGTGGAGATTGGA
ACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTT
GCTTGACCTCTCTGTGCCTCCACTCCCTTAGCTATAAAATGAGCTTACTT

SEQ ID NO:2

FIGURE 2

MRLPGVPLARPALLLLPLLPALLGTGAPAELRVRVRLPDGQVTEESLQADSDADSISLEL
RKPDGTLVSFTADFKKDVKVFRALILGELEKGQSQFQALCFVTQLQHNEIIPSEAMAKLR
QKNPRAVRQAEEVRGLEHLHMDVAVNFSQGALLSPHLHNVCAEAVDAIYTRQEDVRF
WLEQGVDSVFEALPKASEQAELPRCRQVGDRGKPCVCHYGLSLAWYPCMLKYCHSR
DRPTYKCGIRSCQKSYSFDFYVPQRQLCLWDEDPYPG*

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FIGURE 3

MRLPGVPLARPALLLLPLLAPLLG TGAPA

[illegible]

[illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

TRANSLATION OF OAFHUMAN [A]																	
1090	1100	1110	1120	1130	1140	1150	1160	1170									
GTGTGGCATCCG	CAGCTGCC	AAGAGTAC	AGCTTTCG	ACTTCTAC	GTGCCCCA	GAGGCAGCT	GTGTCTCT	GGGATGAG	GATCCCTAC								
CACACCGTAG	GCCTCG	ACGGTCTT	CTCGATGT	CGAAGCTG	AAGATGC	ACGGGTCT	CCTCGC	ACAGAC	AGCCTACT								
C	G	I	R	S	C	Q	K	S	Y								
				S	F	D	F	Y	V								
				P	Q	R	Q	L	C								
								L	W								
								D	E								
								D	P								
								Y	P								
TRANSLATION OF OAFHUMAN [A]																	
1180	1190	1200	1210	1220	1230	1240	1250	1260									
AGGCTAGGGT	GGGAGCA	ACCTGGG	CGGGTGG	CTGCTCT	GGGCCC	ACTGCTTT	CACCAGCC	ACTAGAGG	GGGTGG								
TCCGATCCC	ACCTCG	TTGGAC	CCGCCAC	CGGACG	AGACCC	GGGTGAC	GAGAA	GTGGT	CGGTGAT								
G	*																
1270	1280	1290	1300	1310	1320	1330	1340	1350									
GCCTTATTT	CCCTCC	CTCCCC	ACTCCCT	TGGCCCT	AGAGCCT	GGGCCCC	CTCTGG	CCCCAT	CTCACA								
CGGAATAA	AGGGAG	GGGGT	GAGGG	ACCGG	GATCTC	GACCCG	GGGAG	ACCGG	GATAGAG								
1360	1370	1380	1390	1400	1410	1420	1430	1440									
GCAGGGGT	CTCATG	AAGGCA	CCCCAT	TCCCAC	CTGTGC	CTTCTT	GCGGGC	AGAGAG	GAGAGAG								
CGTCCCC	CAGAGT	ACTTCC	GTGGGG	TAGGGT	GACACG	GAAGGA	ACGCCG	CTCTCT	CCCTCT								
1450	1460	1470	1480	1490	1500	1510	1520	1530									
TCCCTCCT	GCATCT	CCCC	TGGAGT	GTTCAC	TTGCAAG	CTGCCAA	AACATG	ATGGCCT	CTGGTT								
AGGGAGG	ACGTAG	AGGGG	ACCTCA	CAAGTGA	ACGTTT	CGACGGT	TTTGTAC	TACCGG	AGACCA								
1540	1550	1560	1570	1580	1590	1600	1610	1620									
ACCCATAA	AGGAGT	CTATAC	CTGGAC	ACCCAC	CTCCCC	CAGACACA	ACTCCCT	TCCCCA	TGCACAC								
TGGGATT	TTTCTC	AGATAT	GGACCT	GTGGGT	GAGGGT	CTGTGTT	GAGGA	AGGGGT	ACGTGT								
1630	1640	1650	1660	1670	1680	1690	1700	1710									
CCCTTCT	ACTCCC	CAACAG	GGGCTC	ACTATC	CCCCAA	GAAGG	AGCTGT	TGGGG	ACCCAC								
GGGAAGG	ATGAGG	GTGTT	TCCC	CGAGT	GATAGG	GGTTT	CTTCT	CGACA	ACCCCT								
1720	1730	1740	1750	1760	1770	1780	1790	1800									
ATTCTCAT	CTCTG	CCCCG	AGGCTG	CCCTGT	GGGG	CAGTGG	AGACCT	CCCCAT	CACTGAG								
TAAGAGT	AGAGAC	CGGGG	CTCCG	ACGAC	ACCCG	CTCACC	TCTGG	AGGGT	AGTGTG								
1810	1820	1830	1840	1850	1860	1870	1880	1890									
ACCTGAG	CGTGT	GCCTC	CAAAAC	AGGCAC	CAGCTC	TTTCC	CTCTTA	GACAGAA	ATATTTT								
TGGACCT	GCAAC	GAGG	TTTTT	GTCCG	TGTCG	AGAA	GGGAG	AGATCT	GTCTTT								
1900	1910	1920	1930	1940	1950	1960	1970	1980									
AAGTACG	AGGAA	AACTT	GAAAT	CCAGAT	TTTTA	ATGCAA	GTATTT	TATCAT	TTTCT								
TTTCTG	CTCTT	TGAACT	TAAAG	GTCTA	AAAT	TACGTT	TCATAA	ATAGTA	AAAGAT								
1990	2000	2010	2020	2030	2040	2050	2060	2070									
ATGAGAC	CCAGAG	TTTGG	AGAAA	ACTTTT	GGCCA	ATGCTG	CCACCT	GATGTG	CAGAA								
TACTCTG	GGTCTC	AAACCT	CTTTT	GAAA	ACCG	TTACG	ACGGT	GGA	CTTCT								
2080	2090	2100	2110	2120	2130	2140	2150	2160									
AACAAGA	AACTTC	GAAAG	CACTAC	TGTGTG	CTCAG	CCATTT	GAGG	AAGGA	AGGAG								
TTGTT																	

FIGURE 5

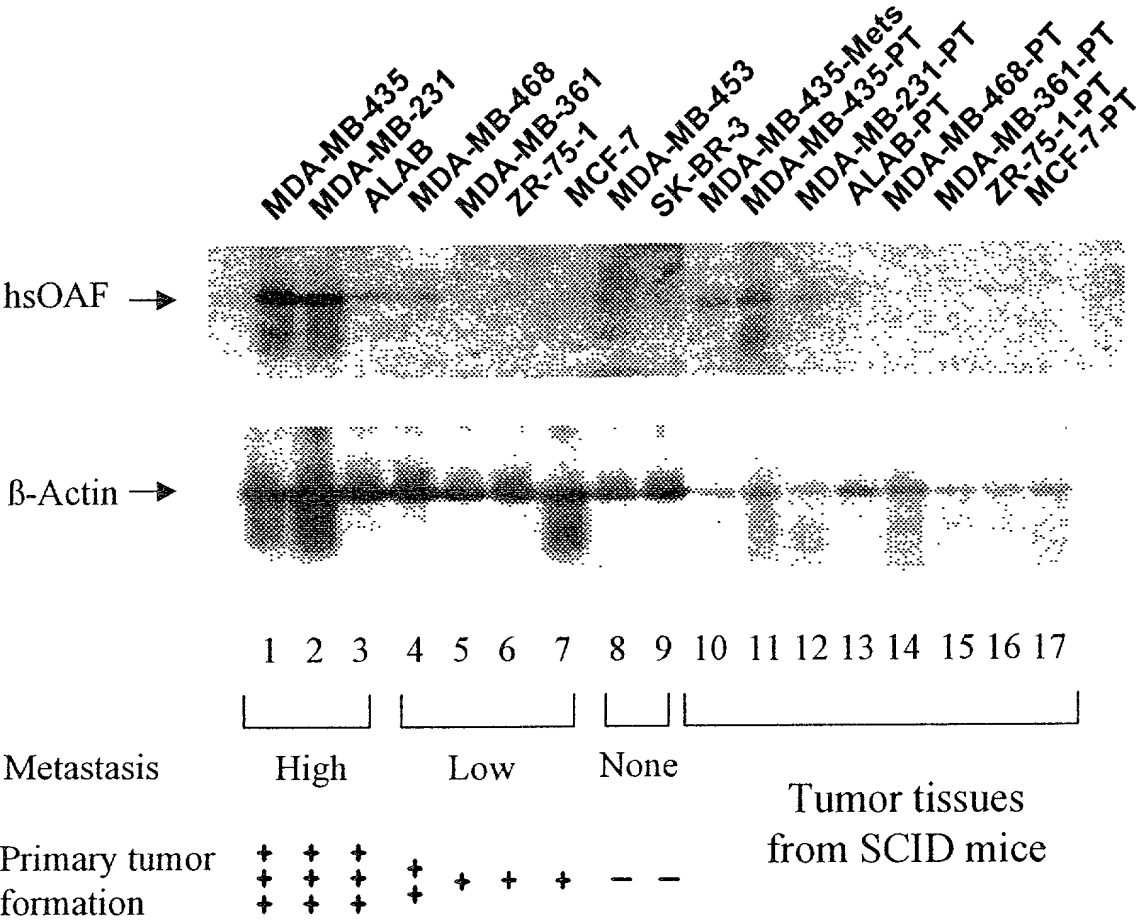


FIGURE 6

MDA-MB-435 soft agar colonies normalized to WST1

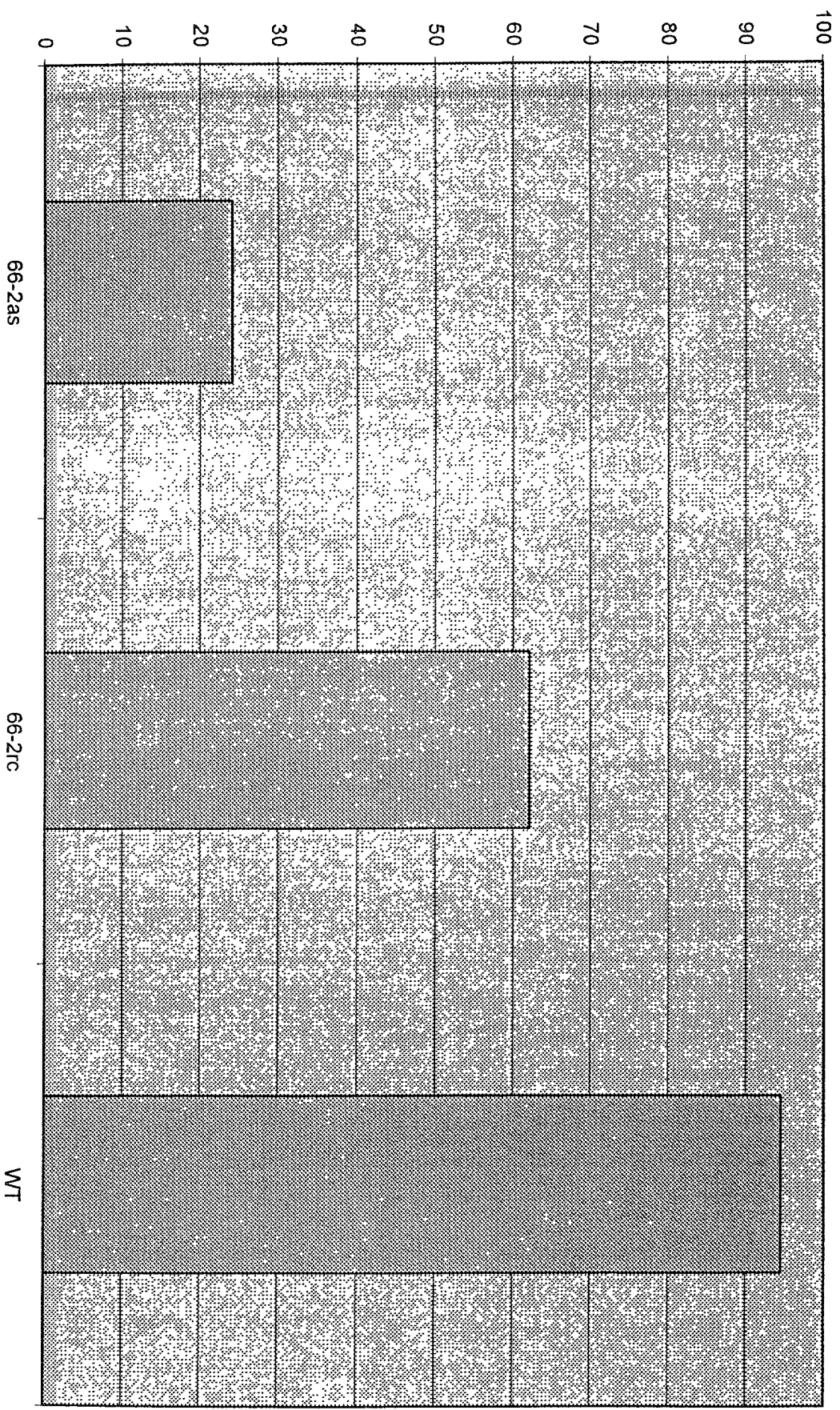


FIGURE 7

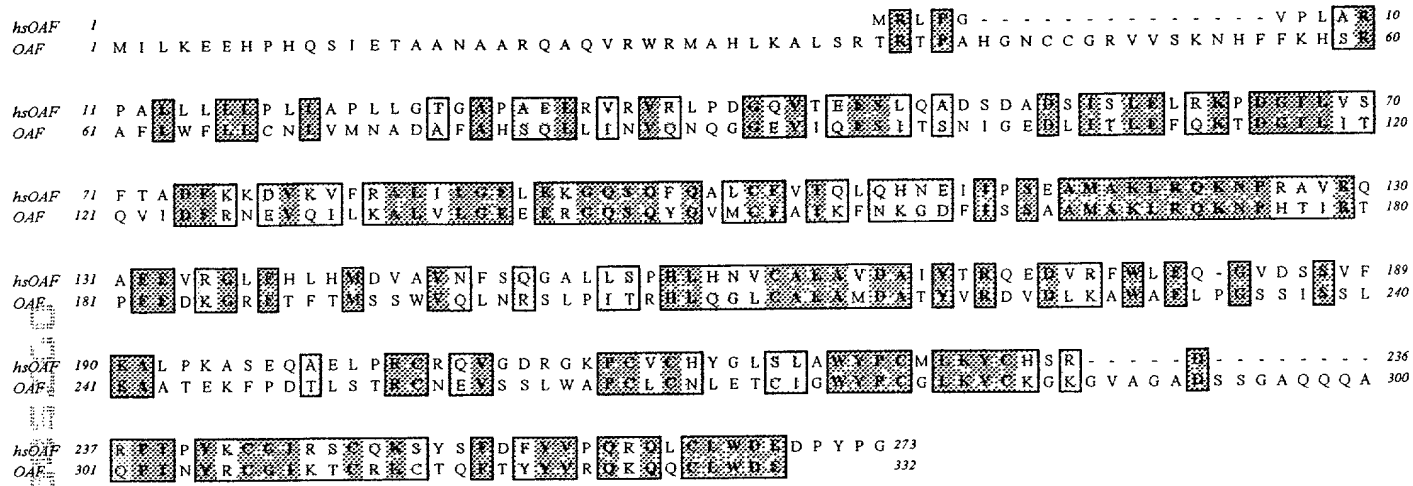


FIGURE 8A

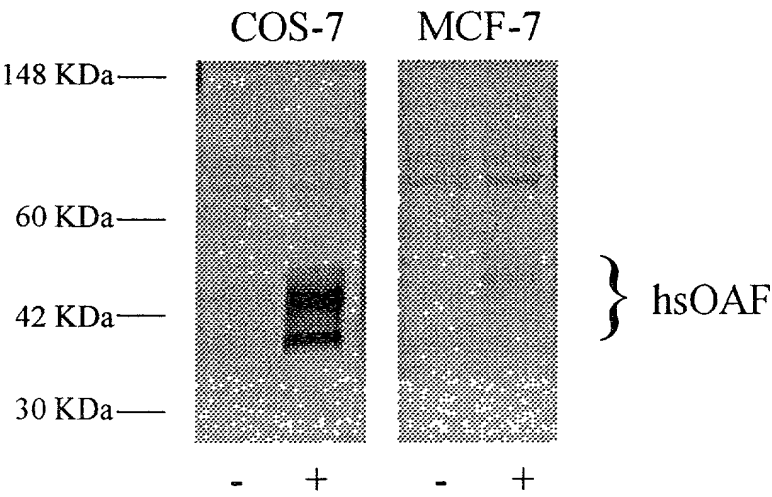


FIGURE 8B

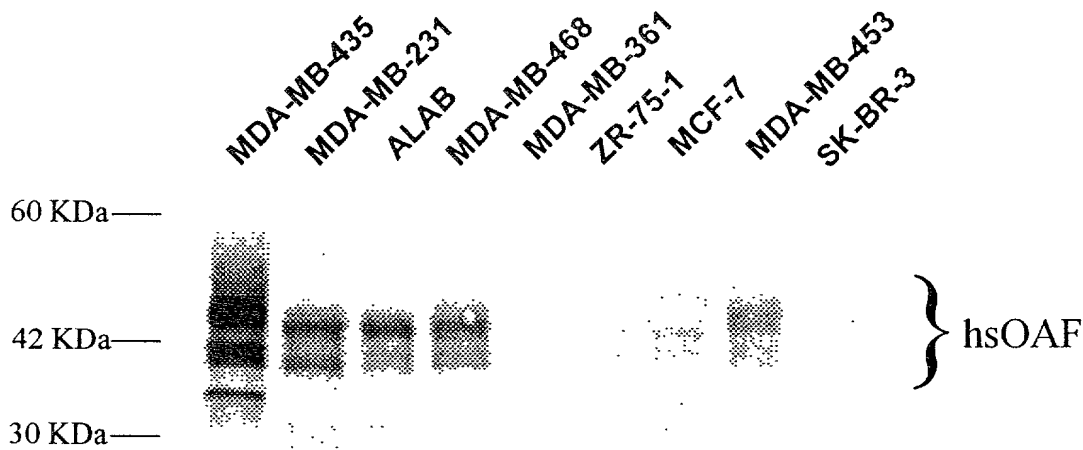


FIGURE 9

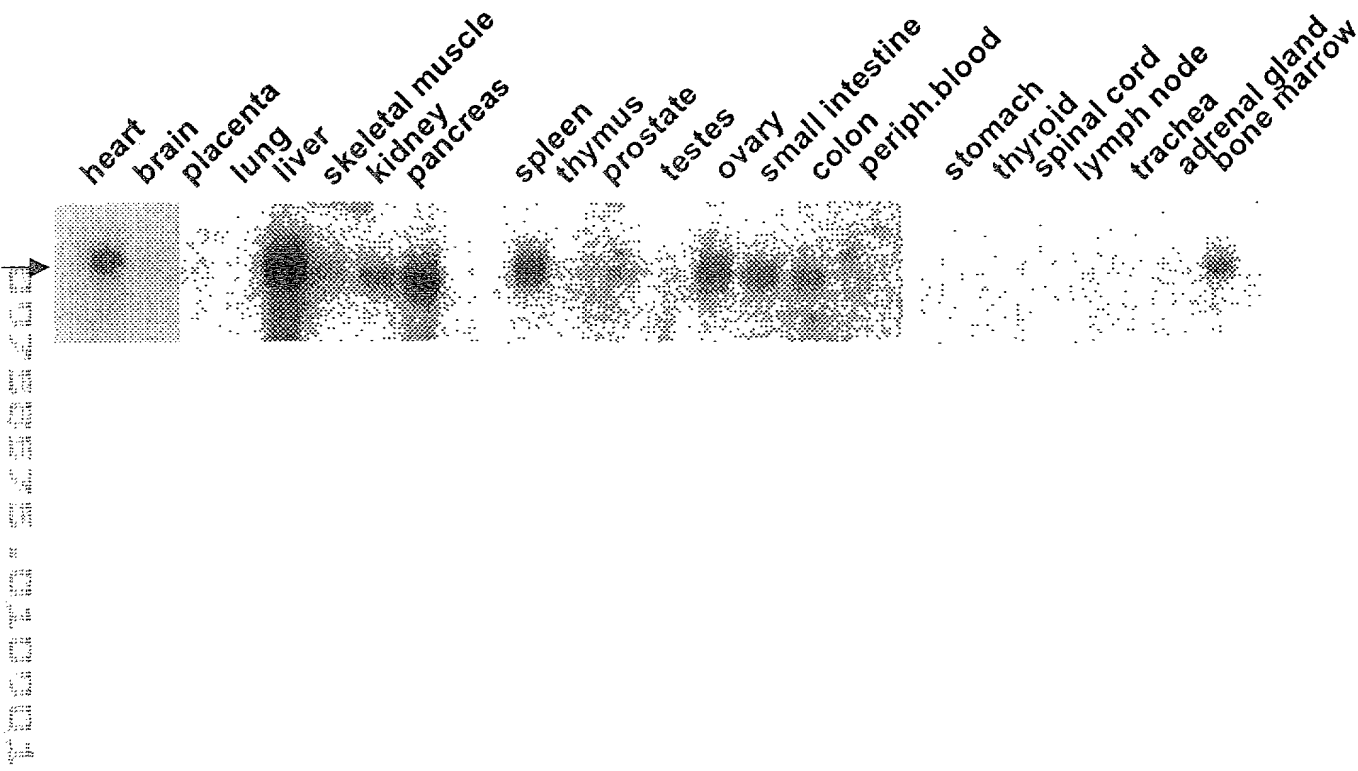
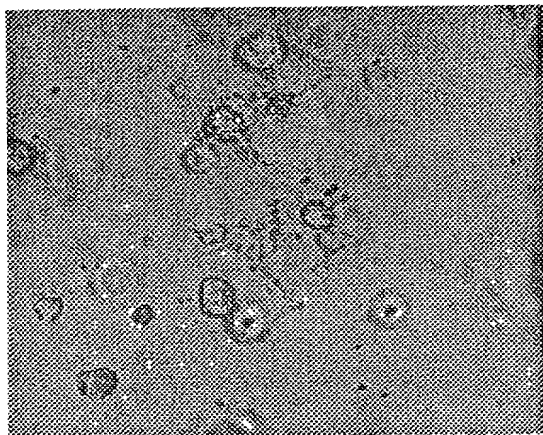
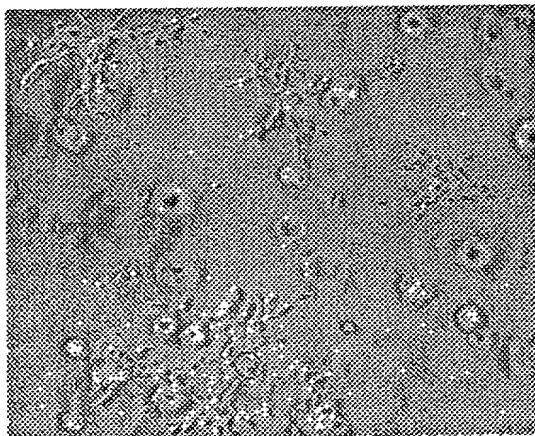


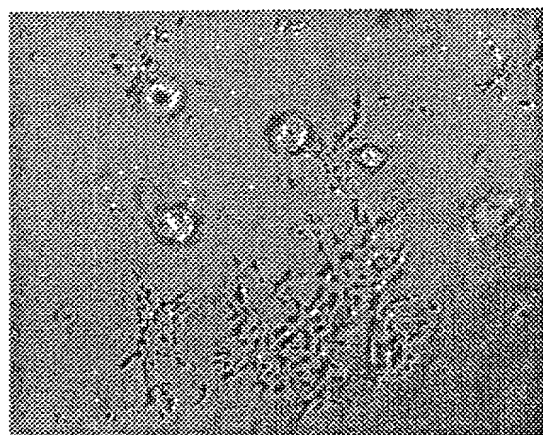
FIGURE 10B



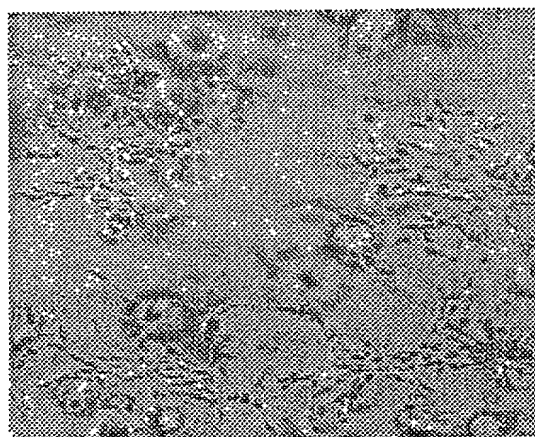
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FIGURE 11

1 CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCTGGTGGTTTCTGTTTCTCTGAAGGAAGTGACGGGGGGTGGGATTGAATGAAAAGTG
 89 CAAAACACAGGCTCGCAGCGCTGGAGCCCCGGGCGCGGAGCCGGGCGGGGCGAGCCCGTCTCCGCCTCGGGGCCGCCGGGGCGCCCT
 179 GCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCGCGGCCAAGGCCCGCGGAGCGGCTCCCGGGCGCCCCGAAGT
 269 AGCCCCAACCTTTGGCGAAGTTTGCTGCGCCTCTCCCCGCCCCACGCGCGCGCGGGGGCGGACGGCAGCGGGCCCCGGGATG
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 359 CGCCTTCCCGGGGTACCCCTGGCGCGCCCTGCGCTGCTGCTGCTGCTGCGCGCTGCTCGCGCGCGTCTGGGAACGGGTGCGCCGGCCGAG
 2 R L P G V P L A R P A L L L L L P L L A P L L G T G A P A E
 449 CTGCGGGTCCGCGTGGCGTGGCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGGACAGCGACGGACAGCATCAGCCTCGAGCTG
 32 L R V R V R L P D G Q V T E E S L Q A D S D A D S I S L E L
 539 CGCAAGCCCCACGGCACCCCTCGTCTCCTTACCGCGGACTTCAAGAAGGATGTGAAGGTCTTCCGGGCCCTGATCTGGGGGAGCTGGAG
 62 R K P D G T L V S F T A D F K K D V K V F R A L I L G E L E
 629 AAGGGGCAGAGTCAGTTCAGGCCCCCTGCTTTGTACCCAGCTGCAGCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGG
 92 K G Q S Q F Q A L C F V T Q L Q H N E I I P S E A M A K L R
 719 CAGAAAAATCCCCGGGCGAGTGGCGGAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTCGCTGTCAACTTCAGCCAGGGG
 122 Q K N P R A V R Q A E E V R G L E H L H M D V A V N F S Q G
 809 GCCCTGCTGAGCCCCCATCTCCACAACTGTGTGCGGAGGCGGTGGATGCCATCTACACCGCCAGGAGGATGTCCGGTTCTGGCTGGAG
 152 A L L S P H L H N V C A E A V D A I Y T R Q E D V R F W L E
 899 CAAGGTGTGGACAGTCTGTGTTTCGAGGCTCTGCCAAGGCCTCAGAGCAGGCGGAGCTGCCTCGCTGCAGGCAGGTGGGGGACCGCGGG
 182 Q G V D S S V F E A L P K A S E Q A E L P R C R Q V G D R G
 989 AAGCCCTGCGCTGCCACTATGGCCTGAGCCTGGCCTGGTACCCCTGCATGCTCAAGTACTGCCACAGCCGCGACCGGCCACGCCCTAC
 212 K P C V C H Y G L S L A W Y P C M L K Y C H S R D R P T P Y
 1079 AAGTGTGGCATCCGAGCTGCCAGAAGAGCTACAGCTTCGACTTCTACGTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTAC
 242 K C G I R S C Q K S Y S F D F Y V P Q R Q L C L W D E D P Y
 1169 CCAGGCTAGGGTGGGAGCAACCTGGCGGGTGGCTGCTCTGGGCCACTGCTCTTACCAGCCACTAGAGGGGGTGGCAACCCCCACCTG
 272 P G *
 1259 AGGCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTAGAGCCTGGGCCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCA
 1349 TGGCAGGGGGTCTCATGAAGGCACCCCATTCACCCTGTGCCCTTCTTGGGGCAGAGAGGGAGAGAAGGGCTCCCCAGATCTACACC
 1439 CCTCCCTCCTGCATCTCCCTGGAGTGTTCACCTTGAAGCTGCCAAAACATGATGGCCTCTGGTGTCTGTGTTGAACCTCTGAACGTTT
 1529 AGACCCATAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACAACCTCCCTTCCCATGCACACATCTGGAAGGAGCTGGCCCCCTCA
 1619 GTCCCTTCTACTCCCAACAAGGGGCTCACTATCCCCAAGAAGGAGCTGTTGGGGACCCACGACGAGCCCTGTACTGGATTACAGC
 1709 ATATTCTCATCTCTGGCCCCGAGGCTGCCGTGGGGCGAGTGGAGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCC
 1799 GGACCTGGACGTGCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTGTAAAGGTCTGGGGCAGGGAGGGAGCA
 1889 TGAAGTACGAGGAAACTTGAATTCAGATTTTTAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTAAAGTTTTACTTGAC
 1979 TAATGAGACCCAGAGTTTGAGAGAAACTTTTGCCCAATGCTGCCACCTGATGTCAGAAAGTGTCCCCACACCTAGCAGTGGCCTATCTT
 2069 GGAACAAGAACTTCGAAAGCACCTACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGAAGGATGAGAT
 2159 AAAACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGTAGTAAGCCAGTCAGAAATAGCCAGCGGAAGGCAAGAGATGGGG
 2249 TGGAGATTGGAACCCGCTTCAGATCTGGGCTCGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTTGCTTGACCTCTCTGTGCCTCCA
 2339 CTCCCTTAGCTATAAAATGAGCTTACTT-polyA

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FIGURE 12A

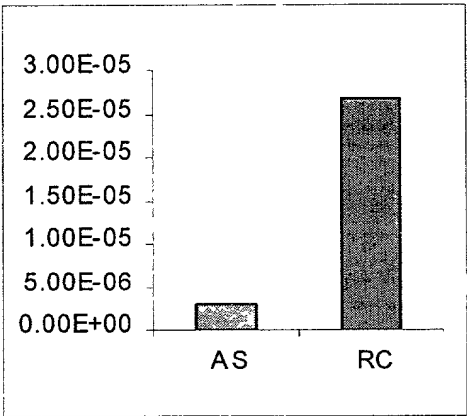


FIGURE 12B

